Amendments to the Specification

Please replace the paragraph beginning at page 6, line 2, with the following rewritten paragraph:

--FIG. 1A shows an alignment of amino acid sequences deduced from cDNAs for CC CKR1 (SEQ ID NO: 9), CC CKR2B (SEQ ID NO: 8), and for CCR5 (SEQ ID NO: 4). Arabic numbers enumerate a CCR5 amino acid sequence (SEQ ID NO:4) and a variant with residue changed from alanine to leucine (SEQ ID NO: 2) that has been deduced from a CCR5 DNA sequence (SEQ ID NO:3 and SEQ ID NO: 1, respectively) and are left-justified. Putative membrane-spanning segments I-VII are noted. Vertical bars show identities between adjacent residues and open boxes show predicted sites for N-linked glycosylation. Dashes and gaps have been inserted to optimize the alignments. Extracellular portions of the CCR5 polypeptide are located between transmembrane domains 2 and 3, transmembrane domains 4 and 5, transmembrane domains 6 and 7, and in the amino terminal segment before transmembrane domain 1.--

Please amend the paragraphs beginning on page 26, line 23 as follows:

--Peptides of the invention include the following which correspond to extracellular loops of CCR5 (amino acid designations are according to the single letter code):
extracellular loop-1 (el-1): A/LAAQWDFGNTMC (SEQ ID NO:[[4]]5)
extracellular loop-2 (el-2): RSQKEGLHYTCSSHFPYSQYQFWK (SEQ ID NO:[[5]]6)
extracellular loop-3 (el-3): QEFFGLNNCSSSNRLD (SEQ ID NO:[[6]]7)
FIG. 2 shows the ability of SEQ ID NO: ~~4, 5 and 6~~ 5, 6, and 7 to inhibit fusion between cells expressing the HIV-1 env (from the macrophage tropic Ba-L isolate) and murine cells co-expressing CD4 and CCR5.--

Please amend the paragraph beginning on page 45, line 27 as follows:

--Seven segments of the deduced amino acid sequence from SEQ ID NO: 1 have a high content of hydrophobic amino acids consistent with membrane-spanning domains as well as multiple amino acids conserved in analogous positions of the known seven-transmembrane-

domain receptor rhodopsin. These considerations clearly indicate that CCR5 is ancestrally related to rhodopsin-like receptors, and strongly suggest that it functions as a seven-transmembrane-domain G protein-coupled receptor. A database search revealed that the highest sequence identity occurs with chemokine receptors. In particular, the amino acid sequence of CCR5 is 57, 70, 75, 51 and 48% identical to CC CKR1, CC CKR2A, CC CKR2B, CC CKR3 and CC CKR4, respectively, with lower identity (approximately 30%) to the CXC chemokine receptors, IL-8 receptors A and B. An alignment of the amino acid sequence of CCR5 ["SEQ ID NO: 2"] with those of CC CKR1 (SEQ ID NO: 9) and CC CKR2B (SEQ ID NO: 8) is shown in ~~Figure~~ FIG. 1A.--

Please amend the paragraphs beginning on page 53, line 10 as follows:

--Synthetic peptides that correspond to the predicted extracellular loops of CCR5 were prepared and tested for inhibition of env-mediated membrane fusion. Peptides were as follows:
extracellular loop-1: LAAQWDFGNTMC (SEQ ID NO:[[4]]5)
extracellular loop-2: RSQKEGLHYTCSSHFPYSQYQFWK (SEQ ID NO:[[5]]6)
extracellular loop-3: QEFFGLNNCSSSNRLD (SEQ ID NO:[[6]]7)--

Please amend the paragraph beginning on page 54, line 8 as follows:

--CCR5 Constructs. Epitope-tagged variants of CCR5 were created to enable detection by the M5 monoclonal antibody (Kodak, Rochester, N.Y.). The CCR5 open reading frame was amplified by PCR using the following primers: 1) for full-length CCR5 (designated CCR5): a 3'-oligonucleotide containing (from 3' to 5') 27 bases complementary to the last 9 codons of CCR5, 3 bases for the stop codon, 6 bases for an Xho I restriction site and 8 miscellaneous bases; 2) for CCR5 lacking most of the cytoplasmic C-terminus (designated $CCR5_{306}$): a 3'-oligonucleotide containing (from 3' to 5') 27 bases complementary to codons 298-306 of CCR5, 3 bases for a stop codon, 6 bases for an *Xho* I restriction site and 8 miscellaneous bases; and 3) for both constructs: a 5'-oligonucleotide containing (from 5' to 3') 8 miscellaneous bases, 6 bases for a Hind III site, 3 bases for the start codon, 24 bases encoding the flag epitope DYKDDDDK (SEQ ID NO: 10) and 27 bases complementary to CCR5 codons 2 to 10. The resulting two PCR products were digested and subcloned between the Hind III and Xho I sites of the changes using a MSIII fluorimeter (Photon Technology International, S. Brunswick, NJ) in HEK 293 cell lines

expressing receptor constructs as previously described. Fuerst, T. R., Niles, E. G., Studier, F. W., and Moss, B. (1986). Briefly, cells were loaded with 2μM FURA-2 AM at 37°C for 45 min, washed twice and resuspended at 10^6 cells/ml in HBSS, pH 7.4. Two ml of the cell suspension were placed in a stirred, water-jacketed cuvette at 37°C and excited sequentially at 340 and 380 nm. Fluorescence emission was monitored at 510 nm before and after addition of agonists. For some experiments, cells were incubated with 250 ng/ml pertussis toxin for 3 h prior to functional assay.--

Please replace pages 1-11 of the sequence listing with enclosed pages 1-12 of the sequence listing.